

Appendix D

Appendix D shows a comparison of the amino acid sequences of the bifunctional LKR-SDH proteins from Arabidopsis, corn and soybean, SEQ ID NOs: 112, 122 and 121, respectively. Amino acids conserved among at least two plant sequences are indicated with an asterisk (*) on the top row; dashes are used by the program to maximize the alignment of the sequences. The LKR and SDH domains (boxed sequences) were identified by Epelbaum et al. (Plant Mol. Biol. 35:735-748 (1997)) and Tang et al. (Plant Cell 9:1305-1316 (1997))

SEQ ID NO:112	MNSNGHEEEKKLGNGVVGILSETVNKWERRTPLTPSHCARLLHGG-KDRTGISRIVVQPS
SEQ ID NO:122	-----CARLLLGGGKNGPRVNRIIVQPS
SEQ ID NO:121	-----
SEQ ID NO:112	AKRIHHDALYEHVGCEISDDLSDCGLILGIKQPELEMILPERAYAFFSHTHKAQKENMPL
SEQ ID NO:122	TRRIHHD AQYEDAGCEISEDLSECGLIIGIKQPKLQMILSDRAYAFFSHTHKAQKENMPL
SEQ ID NO:121	-----
SEQ ID NO:112	LDKILSERVTLC DYELIVGDHGKRL LAFGKYAGRAGLVDFLHGLGQRYLSLGYSTPFLSL
SEQ ID NO:122	LDKILEERVSLFDYELIVGDDGKRS LAFGKFAGRAGLIDFLHGLGQRYLSLGYSTPFLSL
SEQ ID NO:121	-----
LKR domain	
SEQ ID NO:112	GASYMYSSLAAAKAAVISVGEEIASQGLPLGICPLVFVFTGTGNVSLGAQEIFKLLPHTF
SEQ ID NO:122	GQSHMYPSLAAAKAAVIVVAEEIATFGLPSGICPIVFVFTGVGNVSQGAQEIFKLLPHTF
SEQ ID NO:121	-----
SEQ ID NO:112	VEPSKLPELFVKDKGISQNGISTKR VYQVYGCII TSQDMVEHKDPSKSFDKADYYAHPEH
SEQ ID NO:122	VDAEKLPEIF-QARNLSKQSQSTKR V FQLYGCVVTSRDIVSHKDPTRQFDKGDYYAHPEH
SEQ ID NO:121	-----EPKDHVIVFDKADYYSHPEH
SEQ ID NO:112	YNPVFHEKISPYTSVLVNCMYWEKRFPCLLSTKQLQDLTKKGLPLVGICDITCDIGGSIE
SEQ ID NO:122	YTPVFHERIAPYASVIVNCMYWEKRFP LLNMDQLQQLMETGCPLVGVC DITCDIGGSIE
SEQ ID NO:121	YNPTFHEKIAPYASVIVNCMYWEKRFPQLPSYQMQLMGRGSPLVGIADITCDIGGSIE
SEQ ID NO:112	FVNRATLIDSPFFRFNPSNNSYYDDMDGDGVLCMAVDILPTEFAKEASQHF GDILSGFVG
SEQ ID NO:122	FINKSTSIERPFFRYDPSKN SYHDDMEGAGVVCLAVDILPTEFSKEASQHF GNILSRLVA
SEQ ID NO:121	FVNRGTSIDSPFFRYDPLTNSYHDDMEGNVICLAVDILPTEFAKEASQHF GNILSQFVV
SEQ ID NO:112	SLASMT EISDLP AHLKRACISYRGELTSLYEYIPRMRKSNPEEAQDNIIANGVSSQRTFN

SEQ ID NO:122 SLASVKQPAELPSYLRRACIAHAGRLTPLYEYIPMRNTMIDLAPAK--TNPLPDKK-YS
SEQ ID NO:121 NLASATDITKLPAHLRRACIAHKGVLTSLYDYIPMRSSDSEEVSENA-ENSLSNKRKYN

SEQ ID NO:112 ILVSLSGHLFDKFLINEALDMIEAAGGSFHLAKCELGQSADAESYSELEVGGADDKRVLDQ
SEQ ID NO:122 TLVSLSGHLFDKFLINEALDIETAGGSFHLVRCEVGQSTDDMSYSELEVGGADDTATLTK
SEQ ID NO:121 ISVSLSGHLFDQFLINEALDIEAAGGSFHLVNCHVGQSIEAVSFSELEVGGADNRAVLQDQ

SEQ ID NO:112 IIDSLTRLANPNEDYISPHREANKISLKIGKVQQ-ENEIKEKPEMTTKSGVLILGAGRVC
SEQ ID NO:122 IIDSLTSLANEHGGDHDAGQEIE-LALKIGKVNEYETDVTIDKGGPK---ILILGAGRVC
SEQ ID NO:121 IIDSLTAIASPTEHDFRFSNQDSSKISLKLKGVE-ENGIEKESDPRKKA AVLILGAGRVC

SEQ ID NO:112 RPAADFLASVRTISSQQWYKTYFGADSEEKTDVHVIVASLYLKDAKETVEGISDVEAVRL
SEQ ID NO:122 RPAAEFLASYPDICT-----YGVDDHDADQIHVIVASLYQKDAEETVDGIENTTATQL
SEQ ID NO:121 QPAAEMLSSFGRPSSSQWYKTLLEDDFECQTDVEVIVGSLYLKDAEQTVEGIPNVTGIQL

SDH domain

SEQ ID NO:112 DVSDSESLKLYVSQVDVVLSPASCHAVVAKTCIELKKHLVTASYVDDETSMLHEKAKS
SEQ ID NO:122 DVADIGSLSDLVSQVEVVISLLPASFAAIAGVCIELKKHMTASYVDESMSNLSQAQKD
SEQ ID NO:121 DVMDRANLCKYISQVDVVISLLPPSCHIIIVANACIELKKHLVTASYVDSSMSMLNDKAKD

SEQ ID NO:112 AGITILGEMGLDPGIDHMMAMKMINDAHIKKGKVSFTSYCGGLPSPAAANNPLAYKFSW
SEQ ID NO:122 AGVTILCEMGLDPGIDHLSMKMIDEAHARKGKIKAFSTSYCGGLPSPAAANNPLAYKFSW
SEQ ID NO:121 AGITILGEMGLDPGIGHMMAMKMINQAHVRKGKIKSFTSYCGGLPSPAAANNPLAYKFSW

SEQ ID NO:112 NPAGAIRAGQNPACYKSNQDIIHVDGKNLYDSAAFVRPNLPFAFALECFPNRDSLVYGEH
SEQ ID NO:122 NPAGALRSGKNPAVYKFLGETIHVDGHNLYESAKRLRLRELPAFALEHLNPNRNSLIYGD
SEQ ID NO:121 NPAGAIRAGRNPATYKWGGETVHIDGDDLYDSATRLRLPDLPAFALECLPNRNSLLYGD

SEQ ID NO:112 YGIESEATTIFRGTLRYEGFSMIMATLSKLGFFDSEANQVLSTGKRITFGALLSNILNKD
SEQ ID NO:122 YGISKEASTIYRATXRYEGFSEIMVTLSTGFFDAANHPLLQDTSRPTYKGFLELLNNI
SEQ ID NO:121 YGI-TEASTIFRGTLRYEGFSEIMGTLSRISLFNNEAHSLLMNGQRPTFKKFLFELLKVV

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SEQ ID NO:112 ADNESEPLAG----EEEISKRIIKLGHSKE--TAAKAAKTIVFLGFNEEREVPSLCKSV
SEQ ID NO:122 STINTDLIDIEASGGYDDDLIARLLKLGCCNKKEIAVKTVKTIKFLGLHEETQIPKGCSSP
SEQ ID NO:121 GDNPEDELLIG----ENDIMEQILIQGHCKDQRTAMETAKTIIIFLGLLDQTEIPASCKSA

SEQ ID NO:112 FDATECYLMEEKLAYSGNEQDMVLLHHEVEVEFLESKRIEKHTATLLEFGDIKNGQTTTAM
SEQ ID NO:122 FDVICQRMQRMAYGHNEQDMVLLHHEVEVEYPDGQPAEKHQATLLEFGKVENGRSTTAM
SEQ ID NO:121 FDVACFRMEERLSYSTEKDMVLLHHEVEIEYPDSQITEKHRATLLEFGKTLDEKTTTAM

SEQ ID NO:112 AKTVGIPAAIGALVLIEDKIKTRGVLRPLEAEVYLPALDIL-----Q-----
SEQ ID NO:122 ALTVGIPAAIGALLLLKNKVQTKGVIRPLQPEIYVPALEILESSGIKLVKQVET-.KFPD
SEQ ID NO:121 ALTVGIPAAVGALLLLTNKIQTGRVLRPIEPEVYNPALDII-----E-----

<p> ** **** * </p> <p> -----AY-----GIKLME-----KAE.- TQIKI-V.YSRAHVSFVLTPFWNI-YL.-TKM.QIKRTGGVYCKRRQRNLCIYDLSISNN -----AY-----GIKLIE-----KT-E- </p>
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ADQ